Carle	CRF Errors Corrocted by the STIC Systems Branch CRF Processing Usio: 1/2/20 Edited by: Edited by:
	Changed a file from non-ASCII to ASCII
	Changed the margins in cases where the sequence text was "wrapped" down to the next line.
	Edited a lormat error in the Current Application Data section, specifically:
	Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other
	Added the mandatory heading and subheadings for "Current Application Data".
]	Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
	Changed the spelling of a mandatory field (the headings or subheadings), specifically
	Corrected the SEO ID NO when obviously incorrect. The sequence numbers that were edited were:
	Inserted or corrected a nucleic number at the end of a nucleic line. SEO ID NO's edited:
	Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
	Inserted colons after headings/subheadings. Headings edited included:•,
	Deleted extra, invalid, headings-used by an applicant, specifically:
,	Deleted: non-ASCII garbage at the beginning/end of files: secretary initials/filename at end of file: page numbers throughout text; other invalid text, such as
	Inserted mandatory headings, specifically:
	Corrected an obvious erro: in the response, specifically:
	Edited identifiers where upper case is used but lower case is required, or vice versa.
	Corrected an error in the Number of Sequences field, specifically:
	A "Hard Pago Break" code was inserted by the applicant. All occurrences had to be deleted.
(Deloted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patentin bug). Sequences corrected:
	Other:
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